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0606

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/083,620A

DATE: 06/06/2002
TIME: 15:05:43

Input Set : A:\38275.txt
Output Set: N:\CRF3\06062002\J083620A.raw

p.6

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 5 <120> TITLE OF INVENTION: Phosphodiesterase 10
 7 <130> FILE REFERENCE: 27866/38275
 9 <140> CURRENT APPLICATION NUMBER: 10/083,620A
-> 10 <141> CURRENT FILING DATE: 2002-05-30
12 <150> PRIOR APPLICATION NUMBER: 09/256,000
13 <151> PRIOR FILING DATE: 1999-02-23
15 <150> PRIOR APPLICATION NUMBER: 60/075,508
16 <151> PRIOR FILING DATE: 1998-02-23
18 <160> NUMBER OF SEQ ID NOS: 26
20 <170> SOFTWARE: PatentIn Ver. 2.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1548
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (26)..(1423)
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33                             Met Asp Ala Phe Arg Ser Thr Pro Tyr
34                              1               5
36 aaa gtg aga cct gtg gcc atc aag caa ctc tcc gag aga gaa gaa tta   100
37 Lys Val Arg Pro Val Ala Ile Lys Gln Leu Ser Glu Arg Glu Glu Leu
38  10                  15                  20                  25
40 atc cag agc gtg ctg gcg cag gtt gca gag cag ttc tca aga gca ttc   148
41 Ile Gln Ser Val Leu Ala Gln Val Ala Glu Gln Phe Ser Arg Ala Phe
42                  30                  35                  40
44 aaa atc aat gaa ctg aaa gct gaa gtt gca aat cac ttg gct gtc cta   196
45 Lys Ile Asn Glu Leu Lys Ala Glu Val Ala Asn His Leu Ala Val Leu
46              45                  50                  55
48 gag aaa cgc gtg gaa ttg gaa gga cta aaa gtg gtg gag att gag aaa   244
49 Glu Lys Arg Val Glu Leu Glu Gly Leu Lys Val Val Glu Ile Glu Lys
50          60                  65                  70
52 tgc aag agt gac att aag aag atg agg gag gag ctg gcg gcc aga agc   292
53 Cys Lys Ser Asp Ile Lys Lys Met Arg Glu Glu Leu Ala Ala Arg Ser
54      75                  80                  85
56 agc agg acc aac tgc ccc tgt aag tac agt ttt ttg gat aac cac aag   340
57 Ser Arg Thr Asn Cys Pro Cys Lys Tyr Ser Phe Leu Asp Asn His Lys
58  90                  95                  100                 105
60 aag ttg act cct cga cgc gat gtt ccc act tac ccc aag tac ctg ctc   388
61 Lys Leu Thr Pro Arg Arg Asp Val Pro Thr Tyr Pro Lys Tyr Leu Leu
62                 110                 115                 120
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64 tct cca gag acc atc gag gcc ctg cgg aag ccg acc ttt gac gtc tgg   436
65 Ser Pro Glu Thr Ile Glu Ala Leu Arg Lys Pro Thr Phe Asp Val Trp
66             125                 130                 135
68 ctt tgg gag ccc aat gag atg ctg agc tgc ctg gag cac atg tac cac   484
69 Leu Trp Glu Pro Asn Glu Met Leu Ser Cys Leu Glu His Met Tyr His
70         140                 145                 150
72 gac ctc ggg ctg gtc agg gac ttc agc atc aac cct gtc acc ctc agg   532
73 Asp Leu Gly Leu Val Arg Asp Phe Ser Ile Asn Pro Val Thr Leu Arg
74     155                 160                 165
76 agg tgg ctg ttc tgc gtc cac gac aac tac aga aac aac ccc ttc cac   580
77 Arg Trp Leu Phe Cys Val His Asp Asn Tyr Arg Asn Asn Pro Phe His
78 170                 175                 180                 185
80 aac ttc cgg cac tgc ttc tgc gtg gcc cag atg atg tac agc atg gtc   628
81 Asn Phe Arg His Cys Phe Cys Val Ala Gln Met Met Tyr Ser Met Val
82                 190                 195                 200
84 tgg ctc tgc agt ctc cag gag aag ttc tca caa acg gat atc ctg atc   676
85 Trp Leu Cys Ser Leu Gln Glu Lys Phe Ser Gln Thr Asp Ile Leu Ile
86             205                 210                 215
88 cta atg aca gcg gcc atc tgc cac gat ctg gac cat ccc ggc tac aac   724
89 Leu Met Thr Ala Ala Ile Cys His Asp Leu Asp His Pro Gly Tyr Asn
90         220                 225                 230
92 aac acg tac cag atc aat gcc cgc aca gag ctg gcg gtc cgc tac aat   772
93 Asn Thr Tyr Gln Ile Asn Ala Arg Thr Glu Leu Ala Val Arg Tyr Asn
94     235                 240                 245
96 gac atc tca ccg ctg gag aac cac cac tgc gcc gtg gcc ttc cag atc   820
97 Asp Ile Ser Pro Leu Glu Asn His His Cys Ala Val Ala Phe Gln Ile
98 250                 255                 260                 265
100 ctc gcc gag cct gag tgc aac atc ttc tcc aac atc cca cct gat ggg   868
101 Leu Ala Glu Pro Glu Cys Asn Ile Phe Ser Asn Ile Pro Pro Asp Gly
102                270                 275                 280
104 ttc aag cag atc cga cag gga atg atc aca tta atc ttg gcc act gac   916
105 Phe Lys Gln Ile Arg Gln Gly Met Ile Thr Leu Ile Leu Ala Thr Asp
106            285                 290                 295
108 atg gca aga cat gca gaa att atg gat tct ttc aaa gag aaa atg gag   964
109 Met Ala Arg His Ala Glu Ile Met Asp Ser Phe Lys Glu Lys Met Glu
110        300                 305                 310
112 aat ttt gac tac agc aac gag gag cac atg acc ctg ctg aag atg att   1012
113 Asn Phe Asp Tyr Ser Asn Glu Glu His Met Thr Leu Leu Lys Met Ile
114    315                 320                 325
116 ttg ata aaa tgc tgt gat atc tct aac gag gtc cgt cca atg gaa gtc   1060
117 Leu Ile Lys Cys Cys Asp Ile Ser Asn Glu Val Arg Pro Met Glu Val
118 330                 335                 340                 345
120 gca gag cct tgg gtg gac tgt tta tta gag gaa tat ttt atg cag agc   1108
121 Ala Glu Pro Trp Val Asp Cys Leu Leu Glu Glu Tyr Phe Met Gln Ser
122                350                 355                 360
124 gac cgt gag aag tca gaa ggc ctt cct gtg gca ccg ttc atg gac cga   1156
125 Asp Arg Glu Lys Ser Glu Gly Leu Pro Val Ala Pro Phe Met Asp Arg
126            365                 370                 375
128 gac aaa gtg acc aag gcc aca gcc cag att ggg ttc atc aag ttt gtc   1204
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Input Set : A:\38275.txt
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129 Asp Lys Val Thr Lys Ala Thr Ala Gln Ile Gly Phe Ile Lys Phe Val
130         380                 385                 390
132 ctg atc cca atg ttt gaa aca gtg acc aag ctc ttc ccc atg gtt gag   1252
133 Leu Ile Pro Met Phe Glu Thr Val Thr Lys Leu Phe Pro Met Val Glu
134     395                 400                 405
136 gag atc atg ctg cag cca ctt tgg gaa tcc cga gat cgc tac gag gag   1300
137 Glu Ile Met Leu Gln Pro Leu Trp Glu Ser Arg Asp Arg Tyr Glu Glu
138 410                 415                 420                 425
140 ctg aag cgg ata gat gac gcc atg aaa gag tta cag aag aag act gac   1348
141 Leu Lys Arg Ile Asp Asp Ala Met Lys Glu Leu Gln Lys Lys Thr Asp
142                 430                 435                 440
144 agc ttg acg tct ggg gcc acc gag aag tcc aga ggg aga agc aga gat   1396
145 Ser Leu Thr Ser Gly Ala Thr Glu Lys Ser Arg Gly Arg Ser Arg Asp
146             445                 450                 455
148 gtg aaa aac agt gaa gga gac tgt gcc tgaggaaagc ggggggcgtg         1443
149 Val Lys Asn Ser Glu Gly Asp Cys Ala
150         460                 465
152 gctgcagttc tggacgggct ggccgagctg cgcgggatcc ttgtgcaggg aagagctgcc 1503
154 ctgggcacct ggcaccacaa gaccatgttt tctaagaacc atttt                 1548
157 <210> SEQ ID NO: 2
158 <211> LENGTH: 466
159 <212> TYPE: PRT
160 <213> ORGANISM: Homo sapiens
162 <400> SEQUENCE: 2
163 Met Asp Ala Phe Arg Ser Thr Pro Tyr Lys Val Arg Pro Val Ala Ile
164   1               5                  10                  15
166 Lys Gln Leu Ser Glu Arg Glu Glu Leu Ile Gln Ser Val Leu Ala Gln
167             20                  25                  30
169 Val Ala Glu Gln Phe Ser Arg Ala Phe Lys Ile Asn Glu Leu Lys Ala
170         35                  40                  45
172 Glu Val Ala Asn His Leu Ala Val Leu Glu Lys Arg Val Glu Leu Glu
173     50                  55                  60
175 Gly Leu Lys Val Val Glu Ile Glu Lys Cys Lys Ser Asp Ile Lys Lys
176 65                  70                  75                  80
178 Met Arg Glu Glu Leu Ala Ala Arg Ser Ser Arg Thr Asn Cys Pro Cys
179                 85                  90                  95
181 Lys Tyr Ser Phe Leu Asp Asn His Lys Lys Leu Thr Pro Arg Arg Asp
182             100                 105                 110
184 Val Pro Thr Tyr Pro Lys Tyr Leu Leu Ser Pro Glu Thr Ile Glu Ala
185         115                 120                 125
187 Leu Arg Lys Pro Thr Phe Asp Val Trp Leu Trp Glu Pro Asn Glu Met
188     130                 135                 140
190 Leu Ser Cys Leu Glu His Met Tyr His Asp Leu Gly Leu Val Arg Asp
191 145                 150                 155                 160
193 Phe Ser Ile Asn Pro Val Thr Leu Arg Arg Trp Leu Phe Cys Val His
194                 165                 170                 175
196 Asp Asn Tyr Arg Asn Asn Pro Phe His Asn Phe Arg His Cys Phe Cys
197             180                 185                 190
199 Val Ala Gln Met Met Tyr Ser Met Val Trp Leu Cys Ser Leu Gln Glu
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DATE: 06/06/2002
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Input Set : A:\38275.txt
Output Set: N:\CRF3\06062002\J083620A.raw

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200          195                 200                 205
202 Lys Phe Ser Gln Thr Asp Ile Leu Ile Leu Met Thr Ala Ala Ile Cys
203     210                 215                 220
205 His Asp Leu Asp His Pro Gly Tyr Asn Asn Thr Tyr Gln Ile Asn Ala
206 225                 230                 235                 240
208 Arg Thr Glu Leu Ala Val Arg Tyr Asn Asp Ile Ser Pro Leu Glu Asn
209                 245                 250                 255
211 His His Cys Ala Val Ala Phe Gln Ile Leu Ala Glu Pro Glu Cys Asn
212             260                 265                 270
214 Ile Phe Ser Asn Ile Pro Pro Asp Gly Phe Lys Gln Ile Arg Gln Gly
215         275                 280                 285
217 Met Ile Thr Leu Ile Leu Ala Thr Asp Met Ala Arg His Ala Glu Ile
218     290                 295                 300
220 Met Asp Ser Phe Lys Glu Lys Met Glu Asn Phe Asp Tyr Ser Asn Glu
221 305                 310                 315                 320
223 Glu His Met Thr Leu Leu Lys Met Ile Leu Ile Lys Cys Cys Asp Ile
224                 325                 330                 335
226 Ser Asn Glu Val Arg Pro Met Glu Val Ala Glu Pro Trp Val Asp Cys
227             340                 345                 350
229 Leu Leu Glu Glu Tyr Phe Met Gln Ser Asp Arg Glu Lys Ser Glu Gly
230         355                 360                 365
232 Leu Pro Val Ala Pro Phe Met Asp Arg Asp Lys Val Thr Lys Ala Thr
233     370                 375                 380
235 Ala Gln Ile Gly Phe Ile Lys Phe Val Leu Ile Pro Met Phe Glu Thr
236 385                 390                 395                 400
238 Val Thr Lys Leu Phe Pro Met Val Glu Glu Ile Met Leu Gln Pro Leu
239                 405                 410                 415
241 Trp Glu Ser Arg Asp Arg Tyr Glu Glu Leu Lys Arg Ile Asp Asp Ala
242             420                 425                 430
244 Met Lys Glu Leu Gln Lys Lys Thr Asp Ser Leu Thr Ser Gly Ala Thr
245         435                 440                 445
247 Glu Lys Ser Arg Gly Arg Ser Arg Asp Val Lys Asn Ser Glu Gly Asp
248     450                 455                 460
250 Cys Ala
251 465

254 <210> SEQ ID NO: 3
255 <211> LENGTH: 225
256 <212> TYPE: DNA
257 <213> ORGANISM: Homo sapiens
259 <220> FEATURE:
W--> 260 <221> NAME/KEY: misc feature
261 <222> LOCATION: 130
262 <223> OTHER INFORMATION: N = A, T, G, or C
264 <220> FEATURE:
W--> 265 <221> NAME/KEY: misc feature
266 <222> LOCATION: 186
267 <223> OTHER INFORMATION: N = A, T, G, or C
269 <220> FEATURE:
W--> 270 <221> NAME/KEY: misc feature
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/083,620A

DATE: 06/06/2002
TIME: 15:05:43

Input Set : A:\38275.txt
Output Set: N:\CRF3\06062002\J083620A.raw

271 <222> LOCATION: 205
272 <223> OTHER INFORMATION: N = A, T, G, or C
274 <400> SEQUENCE: 3
275 agcgaccgtg agaagtcaga aggccttcct gtggaaccgt tcatggaccg agacaaagtg 60
277 accaaggcca cagcccagat tgggttcatc aagtttgccc tgatcccaat gtttgaaaca 120
W--> 279 gtgaccaagn tcttccccat ggttgaggag atcatgctgc agccactttg ggaatcccga 180
W--> 281 gatcgntacg aggagctgaa gcggntagat gacgccatga aagag 225
284 <210> SEQ ID NO: 4
285 <211> LENGTH: 158
286 <212> TYPE: DNA
287 <213> ORGANISM: Homo sapiens
289 <220> FEATURE:
W--> 290 <221> NAME/KEY: misc feature
291 <222> LOCATION: 12
292 <223> OTHER INFORMATION: N = A, T, G, or C
295 <220> FEATURE:
W--> 296 <221> NAME/KEY: misc feature
297 <222> LOCATION: 37
298 <223> OTHER INFORMATION: N = A, T, G, or C
300 <220> FEATURE:
W--> 301 <221> NAME/KEY: misc feature
302 <222> LOCATION: 62
303 <223> OTHER INFORMATION: N = A, T, G, or C
305 <220> FEATURE:
W--> 306 <221> NAME/KEY: misc feature
307 <222> LOCATION: 110
308 <223> OTHER INFORMATION: N = A, T, G, or C
310 <400> SEQUENCE: 4
W--> 311 gtaccagatc antgcccgca cagagctggc ggtccgntac aatgacatct caccgttgga 60
W--> 313 gnaaccacca ctgcgccgtg gccttccaga tcctcgccga gcctgagtgn aacatcttct 120
315 ccaacatccc acctgatggg ttcaagcaga tccgacag 158
318 <210> SEQ ID NO: 5
319 <211> LENGTH: 98
320 <212> TYPE: DNA
321 <213> ORGANISM: Homo sapiens
323 <220> FEATURE:
W--> 324 <221> NAME/KEY: misc feature
325 <222> LOCATION: 14
326 <223> OTHER INFORMATION: N = A, T, G, or C
328 <220> FEATURE:
W--> 329 <221> NAME/KEY: misc feature
330 <222> LOCATION: 22
331 <223> OTHER INFORMATION: N = A, T, G, or C
333 <220> FEATURE:
W--> 334 <221> NAME/KEY: misc feature
335 <222> LOCATION: 50
336 <223> OTHER INFORMATION: N = A, T, G, or C
338 <400> SEQUENCE: 5
W--> 339 gagaacacca ctgngccgtg gncttccaga tcctcgccga gcctgagtgn aacatcttct 60

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/06/2002
PATENT APPLICATION: US/10/083,620A TIME: 15:05:44

Input Set : A:\38275.txt
Output Set: N:\CRF3\06062002\J083620A.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 130,186,205
Seq#:4; N Pos. 12,37,62,110
Seq#:5; N Pos. 14,22,50
Seq#:6; N Pos. 1,267,352,400,411
Seq#:7; N Pos. 1,82,92,130,347,390,396
Seq#:8; N Pos. 63,98,107,188,203,206,238,252,297,370,389,427
Seq#:11; N Pos. 155,393,442